

RAW SEQUENCE LISTING

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Application Serial Number: 10/542,178
Source: PCT
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/542,178

DATE: 07/21/2005
TIME: 09:41:32

Input Set : A:\HERR-EPAD.00856-03.TXT
Output Set: N:\CRF4\07212005\J542178.raw

3 <110> APPLICANT: University of Virginia Patent Foundation
 4 Herr, John
 5 Allis, C. David
 6 Coonrad, Scott
 7 Wang, Yanming
 9 <120> TITLE OF INVENTION: ePAD, an Oocyte Specific Protein
 11 <130> FILE REFERENCE: 00856-02
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/542,178
 C--> 13 <141> CURRENT FILING DATE: 2005-07-08
 13 <150> PRIOR APPLICATION NUMBER: 60/439,170
 14 <151> PRIOR FILING DATE: 2003-01-10
 16 <150> PRIOR APPLICATION NUMBER: 60/480,774
 17 <151> PRIOR FILING DATE: 2003-06-19
 19 <160> NUMBER OF SEQ ID NOS: 10
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 721
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
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 31 1 5 10 15
 34 Leu Ser Leu Asp Ser Pro Val His Ala Val Cys Val Leu Gly Thr Glu
 35 20 25 30
 38 Ile Cys Leu Asp Leu Ser Gly Cys Ala Pro Gln Lys Cys Gln Cys Phe
 39 35 40 45
 42 Thr Ile His Gly Ser Gly Arg Val Leu Ile Asp Val Ala Asn Thr Val
 43 50 55 60
 46 Ile Ser Glu Lys Glu Asp Ala Thr Ile Trp Trp Pro Leu Ser Asp Pro
 47 65 70 75 80
 50 Thr Tyr Ala Thr Val Lys Met Thr Ser Pro Ser Pro Ser Val Asp Ala
 51 85 90 95
 54 Asp Lys Val Ser Val Thr Tyr Tyr Gly Pro Asn Glu Asp Ala Pro Val
 55 100 105 110
 58 Gly Thr Ala Val Leu Tyr Leu Thr Gly Ile Glu Pro Phe Gly Ala Gln
 59 115 120 125
 62 Arg Ser Ser Ser Gln Ser Phe Val Pro Leu Leu Pro Val Ser Glu Val
 63 130 135 140
 66 Ser Gln Ala Gln Glu Ala Glu Val Ser Leu Glu Val Asp Ile Tyr Arg
 67 145 150 155 160
 70 Asn Gly Gln Val Glu Met Ser Ser Asp Lys Gln Ala Lys Lys Lys Trp
 71 165 170 175
 74 Ile Trp Gly Pro Ser Gly Trp Gly Ala Ile Leu Leu Val Asn Cys Asn

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75	180	185	190
78	Pro Ala Asp Val Gly Gln Gln Leu Glu Asp Lys Lys Thr Lys Lys Val		
79	195	200	205
82	Ile Phe Ser Glu Glu Ile Thr Asn Leu Ser Gln Met Thr Leu Asn Val		
83	210	215	220
86	Gln Gly Pro Ser Cys Ile Leu Lys Lys Tyr Arg Leu Val Leu His Thr		
87	225	230	235
90	Ser Lys Glu Glu Ser Lys Lys Ala Arg Val Tyr Trp Pro Gln Lys Asp		
91	245	250	255
94	Asn Ser Ser Thr Phe Glu Leu Val Leu Gly Pro Asp Gln His Ala Tyr		
95	260	265	270
98	Thr Leu Ala Leu Leu Gly Asn His Leu Lys Glu Thr Phe Tyr Val Glu		
99	275	280	285
102	Ala Ile Ala Phe Pro Ser Ala Glu Phe Ser Gly Leu Ile Ser Tyr Ser		
103	290	295	300
106	Val Ser Leu Val Glu Glu Ser Gln Asp Pro Ser Ile Pro Glu Thr Val		
107	305	310	315
110	320	325	335
111	Leu Tyr Lys Asp Thr Val Val Phe Arg Val Ala Pro Cys Val Phe Ile		
114	330	335	
115	Pro Cys Thr Gln Val Pro Leu Glu Val Tyr Leu Cys Arg Glu Leu Gln		
116	340	345	350
118	Leu Gln Gly Phe Val Asp Thr Val Thr Lys Leu Ser Glu Lys Ser Asn		
119	355	360	365
122	Ser Gln Val Ala Ser Val Tyr Glu Asp Pro Asn Arg Leu Gly Arg Trp		
123	370	375	380
126	Leu Gln Asp Glu Met Ala Phe Cys Tyr Thr Gln Ala Pro His Lys Thr		
127	385	390	395
130	400	405	415
131	Thr Ser Leu Ile Leu Asp Thr Pro Gln Ala Ala Asp Leu Asp Glu Phe		
134	420	425	430
135	Pro Met Lys Tyr Ser Leu Ser Pro Gly Ile Gly Tyr Met Ile Gln Asp		
138	435	440	445
142	Thr Glu Asp His Lys Val Ala Ser Met Asp Ser Ile Gly Asn Leu Met		
143	450	455	460
146	Val Ser Pro Pro Val Lys Val Gln Gly Lys Glu Tyr Pro Leu Gly Arg		
147	465	470	475
150	480	485	495
151	Ser Lys Thr Leu Arg Asp Phe Leu Tyr Ala Gln Gln Val Gln Ala Pro		
154	495	500	510
155	Val Glu Leu Tyr Ser Asp Trp Leu Met Thr Gly His Val Asp Glu Phe		
158	515	520	525
159	Met Cys Phe Ile Pro Thr Asp Asp Lys Asn Glu Gly Lys Lys Gly Phe		
162	530	535	540
166	Leu Leu Leu Ala Ser Pro Ser Ala Cys Tyr Lys Leu Phe Arg Glu		
167	545	550	555
170	Lys Gln Lys Glu Gly Tyr Gly Asp Ala Leu Leu Phe Asp Glu Leu Arg		
171	565	570	575

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174 Leu Leu Ala Asp Glu Ser Leu Lys Lys Gln Asn Glu Tyr Val Glu Cys
 175 580 585 590
 178 Ile His Leu Asn Arg Asp Ile Leu Lys Thr Glu Leu Gly Leu Val Glu
 179 595 600 605
 182 Gln Asp Ile Ile Glu Ile Pro Gln Leu Phe Cys Leu Glu Lys Leu Thr
 183 610 615 620
 186 Asn Ile Pro Ser Asp Gln Gln Pro Lys Arg Ser Phe Ala Arg Pro Tyr
 187 625 630 635 640
 190 Phe Pro Asp Leu Leu Arg Met Ile Val Met Gly Lys Asn Leu Gly Ile
 191 645 650 655
 194 Pro Lys Pro Phe Gly Pro Gln Ile Lys Gly Thr Cys Cys Leu Glu Glu
 195 660 665 670
 198 Lys Ile Cys Cys Leu Leu Glu Pro Leu Gly Phe Lys Cys Thr Phe Ile
 199 675 680 685
 202 Asn Asp Phe Asp Cys Tyr Leu Thr Glu Val Gly Asp Ile Cys Ala Cys
 203 690 695 700
 206 Ala Asn Ile Arg Arg Val Pro Phe Ala Phe Lys Trp Trp Lys Met Val
 207 705 710 715 720
 210 Pro

214 <210> SEQ ID NO: 2

215 <211> LENGTH: 2166

216 <212> TYPE: DNA

217 <213> ORGANISM: Homo sapiens

219 <400> SEQUENCE: 2

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 224 gccccccaga agtgcacgtg cttcaccatc catgctctg ggagggtctt gatcgatgtg 180
 226 gccaacacgg tgatttctga gaaggaggac gccacatct ggtggccct gtctgatccc 240
 228 acgtacgcca cagtgaagat gacatcgccc agcccttccg tggatgcgga taaggtctcg 300
 230 gtcacatact atggggccaa cgaggatgcc cccgtggca cagctgtct gtacacta 360
 232 ggcattgaac ctttggagc tcagaggagc tcttctcgt ctttgcctt gctgcttcca 420
 234 gtcagtgaag tgtctcaggc tcagggaggc gaggtctctc tagaggtaga catctaccgc 480
 236 aatgggcaag ttgagatgtc aagtgcacaaa caggtaaga aaaaatggat ctgggtccc 540
 238 agcggttgg gtgcacatct gcttgcata tgcaacccctg ctgatgtggg ccagcaactt 600
 240 gaggacaaga aaaccaagaa agtgcacatct tcagaggaaa taacgcacatct gtcccacatg 660
 242 actctgaatg tccaaggccc cagctgtatc ttcaaggaaa atcggctatc cttccatacc 720
 244 tccaaggaag agtgcacatg ggcgcacatc tactggccccc aaaaagacaa ctccacatc 780
 246 tttgagttgg tgctggggcc cgaccagcac gcctataacct tggccctctt cgggaaccac 840
 248 ttgaaggaga ctttctcgt tgaagctata gcattccat ctggcgatctt ctcaggcctc 900
 250 atctccatct ctgtgtccct ggtggaggag tctcaagacc cgtcaatcc agagactgtg 960
 252 ctgtacaaag acacgggtt gttccgggtt gtcctgtt tcttcattcc ctgtacccat 1020
 254 gtgcctctgg aggttacatc gtgcacggag ctgcacatgc agggtttgc ggacacatgt 1080
 256 acgaagctga gtgagaagag caacagccag gtggcatctg tctatgagga ccccaaccgc 1140
 258 ctggcaggt ggctccagga tgagatggcc ttctgcata cccaggctcc ccacaagaca 1200
 260 acgtccttga tcctcgacac acctcaggcc gcccgtatctc atgagttccc catgaagtac 1260
 262 tcactgagcc ctggatattgg ctacatgatc caggacactg aggaccataa agtggccagc 1320
 264 atggatttca ttggaaacct gatgggttcc ccacccgtca aggtccaagg gaaagagtac 1380
 266 ccgctggcc gagtccat tggcagcagc ttatccccca ggcgcagaggc ccggccatg 1440
 268 agtaagaccc tccgagactt cctctatgcc cagcaggtcc aagcgccggg ggagctctac 1500

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270	tcagattggc	taatgactgg	ccacgtggat	gagttcatgt	gcttcatccc	cacagatgac	1560									
272	aagaatgagg	gcaaaaaggg	cttcctgctg	ctcctggcca	gccccagtc	ctgtataaa	1620									
274	ctgttccgag	agaaaacagaa	gaaaggctat	ggcgacgctc	ttctgttga	tgagcttaga	1680									
276	gcagatcagc	tcctgtctaa	tggaaggggaa	gccaaaacca	tcgaccaact	tctggctgat	1740									
278	gaaagcctga	agaagcagaa	tgaatacgtg	gagtgcattc	acctgaaccg	tgacatcctg	1800									
280	aagacggagc	tgggcctggt	ggaacaggac	atcatcgaga	ttccccagct	gttctgcttg	1860									
282	gagaagctga	ctaacatccc	ctctgaccag	cagcccaaga	ggtccttgc	gaggccatac	1920									
284	ttccctgacc	tgttgcggat	gattgtgatg	ggcaagaacc	tggggatccc	caagccttt	1980									
286	gggccccaaa	tcaaggggac	ctgctgcctg	gaagaaaaga	tttgctgctt	gctggagccc	2040									
288	ctgggcttca	agtgcacctt	catcaatgac	tttgactgtt	acctgacaga	ggtcggagac	2100									
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306	Lys	Cys	Lys	Ser	Phe	Thr	Ile	Arg	Gly	Ser	Pro	Arg	Ile	Leu	Ile	His
307					20			25								30
310	Ile	Ser	Ser	Ser	Val	Ile	Ala	Gly	Lys	Glu	Asp	Thr	Val	Val	Trp	Arg
311						35			40							45
314	Ser	Met	Asn	His	Pro	Thr	Val	Ala	Leu	Val	Arg	Met	Val	Ala	Pro	Ser
315		50					55				60					
318	Pro	Thr	Val	Asp	Glu	Asp	Lys	Val	Leu	Val	Ser	Tyr	Phe	Cys	Pro	Asp
319	65				70			75								80
322	Gln	Glu	Val	Pro	Thr	Ala	Thr	Ala	Val	Leu	Phe	Leu	Thr	Gly	Ile	Glu
323						85			90							95
326	Ile	Ser	Leu	Glu	Ala	Asp	Ile	Tyr	Arg	Asp	Gly	Gln	Leu	Asp	Met	Pro
327						100			105							110
330	Ser	Asp	Lys	Gln	Ala	Lys	Lys	Trp	Met	Trp	Gly	Met	Asn	Gly	Trp	
331						115			120							125
334	Gly	Ala	Ile	Leu	Leu	Val	Asn	Cys	Ser	Pro	Asn	Ala	Val	Gly	Gln	Pro
335						130			135							140
338	Asp	Glu	Gln	Ser	Phe	Gln	Glu	Gly	Pro	Arg	Glu	Ile	Gln	Asn	Asn	Leu
339	145					150				155						160
342	Ser	Gln	Met	Asn	Val	Thr	Val	Glu	Gly	Pro	Thr	Ser	Ile	Leu	Gln	Asn
343							165			170						175
346	Tyr	Gln	Leu	Ile	Leu	His	Thr	Ser	Glu	Glu	Glu	Ala	Lys	Lys	Thr	Arg
347							180			185						190
350	Val	Tyr	Trp	Ser	Gln	Arg	Gly	Ser	Ser	Ala	Tyr	Glu	Leu	Val	Val	Gly
351						195			200							205
354	Pro	Asn	Lys	Pro	Val	Tyr	Leu	Leu	Pro	Thr	Phe	Glu	Asn	Arg	Arg	Lys
355							210			215						220
358	Glu	Ala	Phe	Tyr	Val	Glu	Ala	Thr	Glu	Phe	Pro	Ser	Pro	Ser	Phe	Ser
359	225					220				235						240
362	Gly	Leu	Ile	Ser	Leu	Ser	Leu	Ser	Leu	Val	Glu	Lys	Ala	His	Asp	Glu
363						245				250						255

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366 Cys Ile Pro Glu Ile Pro Leu Tyr Lys Asp Thr Val Met Phe Arg Val
 367 260 265 270
 370 Ala Pro Tyr Ile Phe Met Pro Ser Thr Gln Met Pro Leu Glu Val Tyr
 371 275 280 285
 374 Leu Cys Arg Glu Leu Gln Leu Gln Gly Phe Val Asp Ser Val Thr Lys
 375 290 295 300
 378 Leu Ser Glu Lys Ser Lys Val Gln Val Val Lys Val Tyr Glu Asp Pro
 379 305 310 315 320
 382 Asn Arg Gln Ser Lys Trp Leu Gln Asp Glu Met Ala Phe Cys Tyr Thr
 383 325 330 335
 386 Gln Ala Pro His Lys Thr Val Ser Leu Ile Leu Asp Thr Pro Arg Val
 387 340 345 350
 390 Ser Lys Leu Glu Asp Phe Pro Met Lys Tyr Thr Leu Thr Pro Gly Ser
 391 355 360 365
 394 Gly Tyr Leu Ile Arg Gln Ile Glu Asp His Arg Val Ala Ser Leu Asp
 395 370 375 380
 398 Ser Ile Gly Asn Leu Met Val Ser Pro Pro Val Lys Ala Gln Gly Lys
 399 385 390 395 400
 402 Asp Tyr Pro Leu Gly Arg Val Leu Ile Gly Gly Ser Phe Tyr Pro Ser
 403 405 410 415
 406 Ser Glu Gly Arg Asp Met Asn Lys Gly Leu Arg Glu Phe Val Tyr Ala
 407 420 425 430
 410 Gln Gln Val Gln Ala Pro Val Glu Leu Phe Ser Asp Trp Leu Met Thr
 411 435 440 445
 414 Gly His Met Asp Gln Phe Met Cys Phe Val Pro Thr Asn Asp Lys Asn
 415 450 455 460
 418 Asn Asp Gln Lys Asp Phe Arg Leu Leu Ala Ser Pro Ser Ala Cys
 419 465 470 475 480
 422 Phe Glu Leu Phe Glu Gln Lys Gln Lys Glu Gly Tyr Asn Val Thr
 423 485 490 495
 426 Leu Phe Glu Asp Ile Gly Ala Glu Gln Leu Leu Ser Asn Gly Arg Glu
 427 500 505 510
 430 Ser Lys Thr Ile Ser Gln Ile Leu Ala Asp Lys Ser Phe Arg Glu Gln
 431 515 520 525
 434 Asn Thr Tyr Val Glu Lys Cys Ile Ser Leu Asn Arg Thr Leu Leu Lys
 435 530 535 540
 438 Thr Glu Leu Gly Leu Glu Asp Lys Asp Ile Ile Leu Ile Pro Gln Leu
 439 545 550 555 560
 442 Phe Cys Leu Glu Gln Leu Thr Asn Val Pro Ser Asn Gln Gln Ser Thr
 443 565 570 575
 446 Lys Leu Phe Ala Arg Pro Tyr Phe Pro Asp Met Leu Gln Ile Ile Val
 447 580 585 590
 450 Leu Gly Lys Asn Leu Gly Ile Pro Lys Pro Phe Gly Pro Lys Ile Asn
 451 595 600 605
 454 Gly Thr Cys Cys Leu Glu Glu Lys Val Cys Gly Leu Leu Glu Pro Leu
 455 610 615 620
 458 Gly Leu Lys Cys Thr Phe Ile Asp Asp Phe Asp Cys Tyr Leu Ala Asn
 459 625 630 635 640
 462 Ile Gly Asp Val Cys Ala Ser Ala Ile Asn Arg Val Pro Phe Ala

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date